

5' C CGC TGC AGC CGC TTT CTG CGG CCT GGG CCT CTC GGC GTC AGC ATG CCA CAC 54
M P H

63 72 81 90 99 108
GCC TTC AAG CCC GGG GAC TTG GTG TTC GCT AAG AAG GGC TAC CCT CAC TGG
A F K P G D L V F A K M K G Y P H W

117 126 135 144 153 162
CCT GCC AGG ATC GAC GAC ATC GCG GAT GGC GCC AAG CCC CCA CCC AAC AAG
P A R I D D I A D G A V K P P P N K

171 180 189 198 207 216
TAC CCC ATC TTT TTC GGC ACA CAC GAA ACA GCC TTC CTG GGC CCC AAA GAC
Y P I F F F G T H E T A F L G P K D

225 234 243 252 261 270
CTC TTC CCT TAC GAG GAA TCC AAG GAG AAG TTT GGC AAG CCC AAC AAG AGG AAA
L F P Y E E S K E K F G G K P N K R K

279 288 297 306 315 324
GGG TTC AGC GAG GGG CTG TGG GAG ATC GAG AAC AAC CCT ACT GTC AAG GCT TCC
G F S E G L W E I E N N P T V K A S

333 342 351 360 369 378
GGC TAT CAG TCC TCC CAG AAA AAG AGC TGT GTG GAA GAG CCT GAA CCA GAG CCC
G Y Q S S Q K K S C V E E P E P

FIGURE 1A

387	GAA GCT GCA GAG GGT GAC GGT GAT AAG AAG GGG AAT GCA GAG GGC AGC AGC GAC	405	414	423	432
	E A A E G D G D K K G N A E G S D				
441	GAG GAA GGG AAG CTG GTC ATT GAT GAG CCA GCC AAG GAG AAG AAC GAG AAA GGA	459	468	477	486
	E E G K L V I D E P A K E K N E K G				
495	GCG TTG AAG AGG AGA GCA GGG GAC TTG CTG GAG GAC TCT CCT AAA CGT CCC AAG	513	522	531	540
	A L K R R A G D L L E D S P K R P K				
549	GAG GCA GAA AAC CCT GAA GGA GAG AAG GAG GCA GCC ACC TTG GAG GTT GAG	567	576	585	594
	E A E N P E G G E K E A A T L E V E				
603	AGG CCC CTT CCT ATG GAG GTG GAA AAG AAT AGC ACC CCC TCT GAG CCC GGC TCT	621	630	639	648
	R P L P M E V E K N S T P S E P G S				
657	GGC CGG GGG CCT CCC CNN NNN NNN NNN NNN NNN NNN NAG GAA GAG GCT	666	675	684	702
	G R G P P P X X X X X X X X X X E A				
711	ACC AAG GAA GAT GCT GAG GCC CCA GGC ATC AAG AGT CAT GAG AGC CTG TAG CCA	720	729	738	756
	T K E D A E A P G I K S H E S L				

FIGURE 1B

765	774	783	792	801	810
CCA ATG TTT CAA GAG GAG CCC CCA CCC TGT TCC TGC TGC TGT CTG GGT ACT					
819	828	837	846	855	864
GGG GAA ACT GGC CAT GGG CTG CAA ACT GGG NAC CCC TTT TCC ANC NCA ANC TGN					

FIGURE 1C

1 M P H A - - - - F K P G D L V F A K M K G Y P H W P A R I D D I A D G A V K P 876242
1 M S R S N R Q K E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S GI 598956
1 M S R S N R Q K E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S GI 945419

36 P P N K Y P I F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K 876242
41 T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K GI 598956
41 T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K GI 945419

76 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E A A E 876242
81 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E A A E GI 598956
81 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C A A E P E V E P E A H E GI 945419

116 G D G D K K G N A E G S S D E E G K L V I D E P A K E K N E K G A L K R R A G D 876242
121 G D G D K K G N A E G S S D E E G K L V I D E P A K E K N E K G A L K R R A G D GI 598956
121 G D G D K K G S A E G S S D E E G K L V I D E P A K E K N E K G T L K R R A G D GI 945419

156 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T 876242
161 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T GI 598956
161 V L E D S P K R P K E S G D H E E D K E I A A L E G E R H L P V E V E K N S T GI 945419

196 P S E P G S G R G P P X X X X X X X X E E A T K E D A E A P G I K S H E S L 876242
201 P S E P G S G R G P P Q E E E E E E D E E E E A T K E D A E A P G I R D H E S L GI 598956
201 P S E P D S G Q G P P A E E E E G E - - - E E A A K E E A E A P G V R D H E S L GI 945419

FIGURE 2

1 CCGCTGCAAGCCGGCTTTCTGCGGCTGGGCTCTCGCGCTC n876242
1 ATGTCGCGA-----TCCAACTCGGC g598956

41 AGCATGCCACACGGCCCTTCAAGCCCGGGGACCTTGGTGTTCG n876242
20 AGAAGGA-GTAC-----AATGCGGGGACCTGGTGTTCG g598956

81 CTAAAGATGAAGGGCTACCCCTCACTGGCCCTGCCAGGATCGA n876242
53 CCAAGATGAAGGGCTACCCCACTGGCCGCGCGATTTGA g598956

121 CGACATCGCGGATGGCGCGCGGTGAAGCCCGCAACAAG n876242
93 CGAATGCTGAAGCTGCGCGTGAATCAAGCCCAACAAG g598956

161 TACCCCATCTTTTCTTTTGGCCACACCGAACAAGCTTCC n876242
133 TACCAGTCTTTTTCGGGACCCACGAGACGCTTCC g598956

201 TGGGCCCCCAAAGACCTCTTCCCTTACGAGGAATCCAGGA n876242
173 TGGGCCCCCAAAGACCTCTTCCCTTACGAGGAATCCAGGA g598956

241 GAAGTTTGGGCAAGCCCAACAAGAGGAAGGGTTCAAGCGAG n876242
213 GAAGTTTGGGCAAGCCCAACAAGAGGAAGGGTTCAAGCGAG g598956

281 GGGCTGTGGGAGATCGAGAACCAACCTACTGTCAAGGCTT n876242
253 GGGCTGTGGGAGATCGAGAACCAACCTACTGTCAAGGCTT g598956

321 CCGGCTATCAGTCCCTCCAGAAAGAGCTGTGTGAAGA n876242
293 CCGGCTATCAGTCCCTCCAGAAAGAGCTGTGTGAAGA g598956

FIGURE 3A

361 G C C T G A A C C A G A G C C C G A A G C T G C A G A G G G T G A C G G T G A T n876242
333 G C C T G A A C C A G A G C C C G A A G C T G C A G A G G G T G A C G G T G A T g598956

401 A A G A A G G G G A A T G C A G A G G G C A G C A G C A G A A G G A n876242
373 A A G A A G G G G A A T G C A G A G G G C A G C A G C A G A A G G A g598956

441 A G C T G G T C A T T G A T G A T G A G C C A G C C A A G G A G A A C G A G A A n876242
413 A G C T G G T C A T T G A T G A T G A G C C A G C C A A G G A G A A C G A G A A g598956

481 A G G A G C G T T G A A G A G G A G A G C A G G G G A C T T G C T G G A G G A C n876242
453 A G G A G C G T T G A A G A G G A G A G C A G G G G A C T T G C T G G A G G A C g598956

521 T C T C C T A A A C G T C C C A A G G A G G C A G A A A A C C C T G A A G G A G n876242
493 T C T C C T A A A C G T C C C A A G G A G G C A G A A A A C C C T G A A G G A G g598956

561 A G G A G A A G G A G G C A G C C A C C T T G G A G G T T G A G A G C C C T n876242
533 A G G A G A A G G A G G C A G C C A C C T T G G A G G T T G A G A G C C C T g598956

601 T C C C T A T G G A G G T G G A A A A G A A T A G C A C C C C C T C T G A G C C C n876242
573 T C C C T A T G G A G G T G G A A A A G A A T A G C A C C C C C T C T G A G C C C g598956

641 G G C T C T G G C C C G G G G C C T C C C C N N N N N N N N N N N N n876242
613 G G C T C T G G C C C G G G G C C T C C C C A A G A G G A A G A A G A G A G g598956

FIGURE 3B

681 NNNNNNNNAGGAAGAGGCTACCAAGGAAGATTGCTGAGGC n876242
 653 AGGATGAAGAGGAAGAGGCTACCAAGGAAGATTGCTGAGGC g598956

 721 CCCAGGCATCAAGAGTCAATGAGAGCCCTGTAGCCCATG n876242
 693 CCCAGGCATCAGAGATCAATGAGAGCCCTGTAG g598956

 761 TTTCAAGAGGAGCCCCCACCCTGTTCTGCTGCTG n876242
 723 g598956

 801 GTGCTACTGGGGAACCTGGGCCATGGGCTGCACAAC TGGGNA n876242
 723 g598956

 841 CCCCCTTTCCANCNCANCTGNTNTCTT n876242
 723 g598956

FIGURE 3C

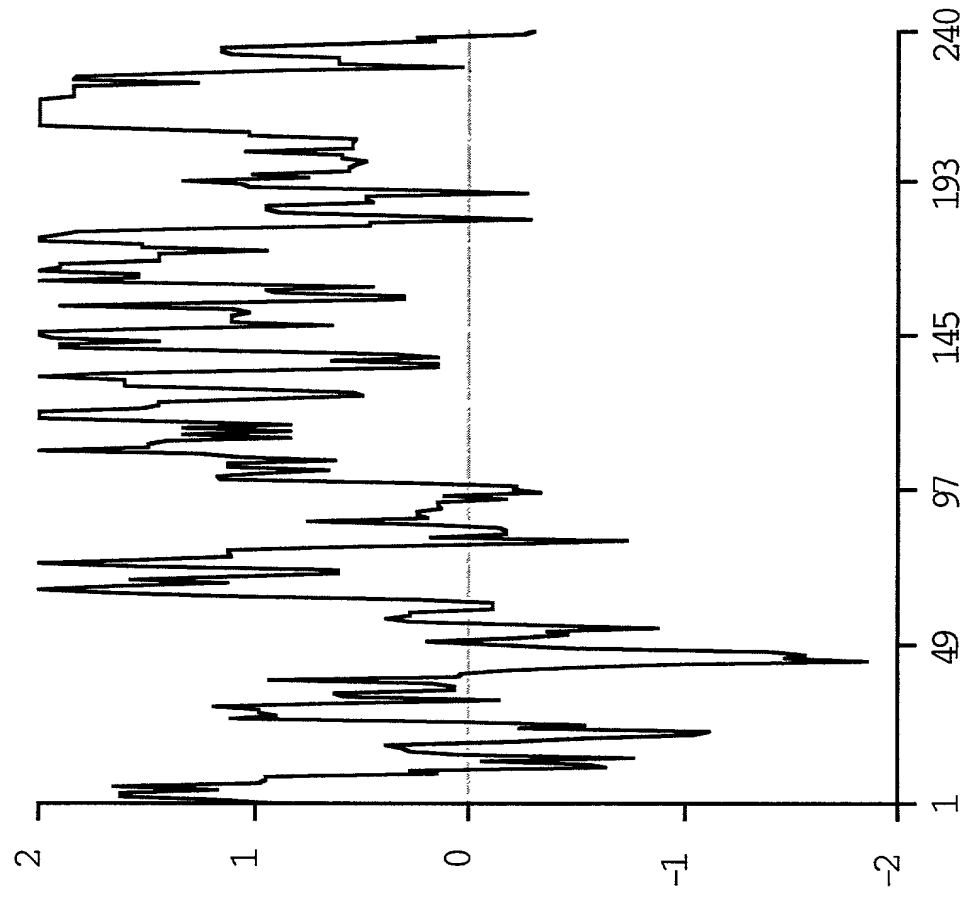


FIGURE 4B

Library	Lib Description	Abun	Pct Abun
HNT3AZT01	hNT2 cell line, teratocarcinoma, treated AZ	5	0.3425
THP1PLB02	THP-1 promonocyte cell line, treated PMA, LPS	4	0.1630
THP1PEB01	THP-1 promonocyte cell line, treated PMA	3	0.1463
PANCDIT03	pancreas, NIDDM, 57 M	1	0.1462
THP1T7T01	THP1 cells, untreated	3	0.1447
BSTMNOT01	brain stem, 72 M	1	0.1214
PROSTUT12	prostate tumor, 65 M, match to PROSNOT20	4	0.1118
HUVESTB01	HUVEC endothelial cell line, shear stress	3	0.1078
PENITUT01	penis tumor, carcinoma, 64 M	4	0.1066
AMLENOT01	AML blast cells, blast crisis, 58 F	1	0.1058
COLNNOT13	colon, ascending, 28 M	3	0.0932
HUVENOB01	HUVEC endothelial cell line, control	2	0.0841
UTRSNOT05	uterus, 45 F	3	0.0834
SINTNOT13	small intestine, ileum, ulcerative cholangitis, 25 F	3	0.0826
LUNGNOT03	lung tumor, 69 M, match to LUNGNOT15	5	0.0796
OVARNOT01	ovary, 49 F, WM	1	0.0752
PLACNOT02	placenta, neonatal F, NORM, WM	13	0.0722
PROSNOT01	prostate, 78 M	2	0.0702
SPLNFEM01	spleen, fetal, WM	2	0.0663
COLNNOT19	large intestine, cecum, 18 F	2	0.0585
PROSTUT05	prostate tumor, 69 M, match to PROSNOT07	4	0.0580
COLNFET02	colon, fetal F	4	0.0571

FIGURE 5A

THP1NOT01	THP1 cells, untreated	1	0.0571
LUNGNOT02	lung tumor, metastasis, 79 M, match to LUNGNOT03	3	0.0567
SININOT01	small intestine, ileum, 4 F	2	0.0560
THP1AZT01	THP-1 promonocyte cell line, treated AZ	1	0.0554
LUNGNOT15	lung, 69 M, match to LUNGNOT03	2	0.0553
LIVRFET02	liver, fetal F	2	0.0550
KERANOT02	keratinocytes, primary cell line, 30 F	3	0.0546
PROSTUT09	prostate tumor, 66 M	2	0.0529
LEUKNOT03	white blood cells, 27 F	2	0.0523
TESTNOT03	testis, 37 M	4	0.0515
COLNPOT01	colon polyp, 40 F	2	0.0513
PROSNOT14	prostate, 60 M, match to PROSTUT08	2	0.0512
BRAITUT02	brain tumor, metastasis, 58 M	3	0.0509
BRSTTUT03	breast tumor, 58 F, match to BRSTNOT05	5	0.0493
TESTNOT01	testis, 37 M	1	0.0478
UCMCNOT02	mononuclear cells	2	0.0471
THP1PLB01	THP-1 promonocyte cell line, treated PMA, LPS	1	0.0452
BRSTNOT02	breast, 55 F, match to BRSTTUT01	4	0.0443
PROSNOT02	prostate, 50 M, match to PROSTUT01	1	0.0435
COLNNOT08	colon, 60 M	1	0.0426
PANCTUT02	pancreatic tumor, carcinoma, 45 F	2	0.0403
SCORNOT01	spinal cord, 71 M	2	0.0402
UTRSNOT01	uterus, 59 F	1	0.0394
SINTTUT01	small intestine tumor, ileum, 42 M	1	0.0382

FIGURE 5B

TLYMNOR01	lymphocytes (non-adher PBMC), 24 M, RP	1	0.0379
HNT2RAT01	hNT2 cell line, teratocarcinoma, treated RA	2	0.0376
BRAINOT03	brain, 26 M	2	0.0371
LUNGNOT04	lung, 2 M	2	0.0366
PROSNOT20	prostate, 65 M, match to PROSTUT12	1	0.0336
CARDFEM01	heart, fetal, NORM, WM	3	0.0335
OVARFUT01	ovarian tumor, 43 F, match to OVARNOT03	1	0.0323
OVARNOT02	ovary, 59 F	1	0.0316
NEUTGMT01	granulocytes, periph blood, M/F, treated GM-CSF	2	0.0313
BRSTNOT05	breast, 58 F, match to BRSTTUT03	2	0.0309
STOMNOT02	stomach, 52 M, match to STOMTUT01	1	0.0308
BRSTNOT07	breast, 43 F	1	0.0307
STOMNOT01	stomach, 55 M	1	0.0303
LUNGNOT18	lung, 66 F	1	0.0298
TONGTUT01	tongue tumor, carcinoma, 36 M	1	0.0295
BRAITUT08	brain tumor, astrocytoma, 47 M	2	0.0293
COLNTUT06	large intestine, cecal tumor, 45 F	1	0.0293
LIVSFEM02	liver/spleen, fetal M, NORM, WM	11	0.0290
BEPINOT01	bronchial epithelium, primary cell line, 54 M	2	0.0289
PANCNOT07	pancreas, fetal M	1	0.0287
UTRSNOT06	uterus, myometrium, 50 F	1	0.0282
LUNGNOT12	lung, 78 M	1	0.0278
TESTTUT02	testicular tumor, 31 M	1	0.0278

FIGURE 5C

THYRTUT03	thyroid tumor, benign, 17 M	1	0.0276
LATRTUT02	heart tumor, myoma, 43 M	2	0.0275
BEPINON01	bronchial epithelium, 1° cell line, 54 M, NORM	1	0.0274
OVARNOT07	ovary, 28 F	1	0.0269
PTHYTUM01	parathyroid tumor, adenoma, M/F, NORM, WM	1	0.0268
KIDNTUT01	kidney tumor, Wilms, 8m F	1	0.0267
LATRNOT01	heart, left atrium, 51 F	1	0.0266
PROSTUT08	prostate tumor, 60 M, match to PROSNOT14	1	0.0266
BRSTNOM01	breast, F, NORM, WM	1	0.0264
BRAITUT13	brain tumor, meningioma, 68 M	1	0.0262
DUODNOT02	small intestine, duodenum, 8 F	1	0.0262
URETTUT01	ureter tumor, 69 M	1	0.0262
BRAITUT07	brain tumor, left frontal, 32 M	1	0.0259
LIVRTUT01	liver tumor, metastasis, 51 F	1	0.0259
PROSNOT18	prostate, 58 M	1	0.0256
PANCNOT08	pancreas, 65 F, match to PANCUTUT01	1	0.0254
BLADTUT04	bladder tumor, 60 M, match to BLADNOT05	2	0.0253
PLACNOB01	placenta, neonatal F	1	0.0251
LUNGNOT02	lung, 47 M	1	0.0246
TMLR3DT02	lymphocytes (non-adher PBMNC), M/F, 72-hr MLR	1	0.0246
HIPONOT01	brain, hippocampus, 72 F	1	0.0239
RATRNOT02	heart, right atrium, 39 M	1	0.0237
MMLR1DT01	macrophages (adher PBMNC), M/F, 24-hr MLR	1	0.0236

FIGURE 5D

TMLR3DT01	lymphocytes (non-adher PBMNC), M, 96-hr MLR	1	0.0229
PROSNOT06	prostate, 57 M, match to PROSTUT04	2	0.0228
LIVRNOT01	liver, 49 M	1	0.0198
COLNTUT03	colon tumor, 62 M, match to COLNNOT16	1	0.0196
CRBLNOT01	brain, cerebellum, 69 M	1	0.0195
CERVNOT01	cervix, 35 F	1	0.0194
BRSTNOT04	breast, 62 F	2	0.0192
MELANOM01	melanocytes, M, NORM, WM	2	0.0192
LUNGAST01	lung, asthma, 17 M	2	0.0189
SYNOOAT01	synovium, knee, osteoarthritis, 82 F	1	0.0180
MMLR2DT01	macrophages (adher PBMNC), M/F, 48-hr MLR	1	0.0178
SYNORAT04	synovium, wrist, rheumatoid, 62 F	1	0.0174
HNT2NOT01	hNT2 cell line, teratocarcinoma, control	1	0.0173
UCMCL5T01	mononuclear cells, treated IL-5	2	0.0168
CONNNOT01	fat, mesentary, 71 M	1	0.0149
BRSTTUT02	breast tumor, 54 F, match to BRSTNOT03	1	0.0140
BRAITUT01	brain tumor, oligoastrocytoma, 50 F	1	0.0134
SINTFET03	small intestine, fetal F	1	0.0130
KIDNNOT05	kidney, neonatal F	1	0.0106
CORPNOT02	brain, corpus callosum, Alzheimer's, 74 M	1	0.0103
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0095
LUNGFET03	lung, fetal F	1	0.0091
BRAINOM01	brain, infant F, NORM, WM	1	0.0045

FIGURE 5E